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RESULT 12
US-09-488-856A-10/c
; Sequence 10, Application US/09488856A
; Patent NO. 6316259
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXP
; FILE REFERENCE: RTS-0115
; CURRENT APPLICATION NUMBER: US/09/488,856A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 12394
; TYPE: DNA
; ORGANISM: Homo sapiens

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RESULT 13
US-08-709-923-1/c
; Sequence 1, Application US/08709923
; Patent No. 5831055
; GENERAL INFORMATION:
; APPLICANT: BIENKOWSKI, MICHAEL J.
; TITLE OF INVENTION: NOVEL KIDNEY ATP-DEPENDENT POTASSIUM
; CHANNELS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn Company
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,923
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootton, Thomas A.
; REGISTRATION NUMBER: 35,004
; REFERENCE/DOCKET NUMBER: 6001.N CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-833-7914

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; TELEFAX: 616-833-6897
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-709-923-1

Query Match          10.6%; Score 106.6; DB 2; Length 2896;
Best Local Similarity 76.9%; Pred. No. 4.4e-22;
Matches 130; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 TGGACGCGGCTGTAGTCCAGCTACTCAGGAGACTGAGGAGAGAAATCGCTTGAACCC 60
Db 169 TGGCATCGGCTGTAGTCCAGCTACTCAGGAGGCTGAGGAGAGAAATCGCTTGAACCC 110
QY 61 GGGAGACGGAGGTTGCAGTCAGGCAAGATCGCTCACTGCCTCCAGCTGGGCAACAC 120
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QY 121 GTTCCGTTTCAAAAGAAAAAATAATTAATAAAAAAGATAAAATCCG 169
Db 49 GGAATAATTCACACTCAAAAGAAAAAGAGAGAGAGATAAGATCAGATCAG 1

RESULT 14
US-08-724-394A-20/c
; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant

; TELEFAX: 616-833-6897
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-724-394A-20

Query Match          10.6%; Score 106.6; DB 2; Length 246240;
Best Local Similarity 81.8%; Pred. No. 6.3e-21;
Matches 135; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

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Db 172447 TGGACATGCTGTAGTCCAGCTACTTGGGAGGCTGAGGAGAGAAATGCTTGAACCTC 172388
QY 61 GGGAGACGGAGGTTGCAGTCAGGCAAGATCGCTCACTGCCTCCAGCTGGGCAACAC 120
Db 172387 GGGAGGCGGAGGTTGCAGTCAGGCGGAGATTGCGCCACTGCCTCCAGCTGGGCAACAC 172329
QY 121 GTTCCGTTTCAAAAGAAAAAATAATTAATAAAAAAGATAAAATA 165
Db 172328 GTGAGACTCCGCTCTAAAAATAATAATAATAATAATAATAATA 172284

RESULT 15
US-08-724-394A-21/c
; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..246240
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; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
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Best Local Similarity 81.8%; Pred. No. 6.3e-21;
Matches 135; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

Qy 1 TGGCAGCGCCCTGTAGTCCCACTACTCAGGAGACTGAGCGAGGAGAAATCGCTTGAACCC 60
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Db 172447 TGGCACATGCCCTGTAGTCCCACTACTGCGGAGGCTGAGGCGAGGAAATTGCTTGAACCTC 172388

Qy 61 GGGAGAGCGGAGGTTGCAGTGAGCCCAAGATCCCGTCACCTGCACCTCCAGCTGGCGACAGAC 120
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Db 172387 GGGAGCGGAGGTTGCAGCGAGCGGAGATTGCGCCACTGCACCTCCAGCTGGTGACAGA- 172329

Qy 121 GTTCCGTTTCAAAAGAAAAAATAATATTAATAAAAGATAAAA 165
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Db 172328 GTGACACTCCGCTCAAAAATAATAATAATAATAATAATAATA 172284
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Search completed: December 24, 2002, 23:36:36
Job time : 489.673 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2002, 21:54:28 ; Search time 32.3575 Seconds
(without alignments)
12277.043 Million cell updates/sec

Title: US-09-708-724A-3_COPY_99000_100000

Perfect score: 1001

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
c 1	117.4	11.7	17792	10	US-09-764-869-1599
	2	115	11.5	601	10 US-09-820-003A-28
	3	115	11.5	46050	10 US-09-820-003A-3
	4	113.6	11.3	30350	9 US-10-118-328-3
	5	113.4	11.3	35414	10 US-09-836-607-45
c 6	113.4	11.3	397658	10	US-09-813-320-3
	7	112.4	11.2	2147	10 US-09-764-847-1738
	8	112.2	11.2	14485	10 US-09-876-216-3
	9	112.2	11.2	95014	10 US-09-880-107-3428
	10	111.2	11.1	2547	10 US-09-764-877-2582
c 12	111.2	11.1	1503841	9	US-09-946-807-1
	12	111.2	11.1	1503841	10 US-09-795-668-1
	13	111.2	11.1	1503841	10 US-09-795-686-1
	14	110.6	11.0	15849	10 US-09-880-107-2362
	15	110.6	11.0	32154	10 US-09-764-877-3433
c 16	110.4	11.0	406	9	US-09-764-868-1475
	17	110.4	11.0	2294	12 US-10-052-586-283
	18	110.4	11.0	31208	10 US-09-852-067-3
	19	110.4	11.0	198285	10 US-09-880-107-3814

c 20	110.2	11.0	145831	10	US-09-969-708-79	Sequence 79, Appl
c 21	110.2	11.0	145831	10	US-09-954-456-2116	Sequence 2116, Ap
c 22	110	11.0	1400	10	US-09-263-959-295	Sequence 295, App
c 23	110	11.0	29695	10	US-09-752-820A-3	Sequence 3, Appli
c 24	110	11.0	29695	10	US-09-813-319A-3	Sequence 3, Appli
c 25	110	11.0	684973	10	US-09-263-959-1	Sequence 1, Appli
c 26	109.8	11.0	57130	10	US-09-835-081-3	Sequence 3, Appli
c 27	109.4	10.9	11991	10	US-09-764-877-2942	Sequence 2942, Ap
c 28	109	10.9	213	9	US-09-860-670-177	Sequence 177, App
c 29	109	10.9	21724	10	US-09-764-864-1603	Sequence 1603, Ap
c 30	109	10.9	21727	10	US-09-764-864-1604	Sequence 1604, Ap
c 31	109	10.9	110096	10	US-09-880-107-1542	Sequence 1542, Ap
c 32	108.6	10.8	248	10	US-09-764-847-1741	Sequence 1741, Ap
c 33	108.6	10.8	3807	10	US-09-764-877-2864	Sequence 2864, Ap
c 34	108.4	10.8	13058	10	US-09-764-846-303	Sequence 303, App
c 35	108.4	10.8	23433	10	US-09-927-091-7	Sequence 7, Appli
c 36	108.4	10.8	30625	10	US-09-927-091-5	Sequence 5, Appli
c 37	108.4	10.8	30676	10	US-09-927-091-8	Sequence 8, Appli
c 38	108.4	10.8	32185	10	US-09-764-877-3171	Sequence 3171, Ap
c 39	108.4	10.8	65608	9	US-09-954-531-180	Sequence 180, App
c 40	108.4	10.8	65608	10	US-09-962-436-292	Sequence 292, App
c 41	108.4	10.8	65608	10	US-09-962-832-119	Sequence 119, App
c 42	108.2	10.8	1807	10	US-09-880-107-2132	Sequence 2132, Ap
c 43	108	10.8	7537	10	US-09-764-869-1735	Sequence 1735, Ap
c 44	108	10.8	145831	10	US-09-969-708-79	Sequence 79, Appl
c 45	108	10.8	145831	10	US-09-954-456-2116	Sequence 2116, Ap

ALIGNMENTS

RESULT 1

US-09-764-869-1599/c
; Sequence 1599, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1599
; LENGTH: 17792
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1599

Query Match		11.7%	Score 117.4;	DB 10;	Length 17792;
Best Local Similarity		81.1%	Pred. No. 8e+22;	31;	Indels 4;
Matches 150;		Conservative 0;	Mismatches	0;	Gaps 1;
QY	1	TGGCAGCGCGCTGTAGTCCCGCTACTCAGGAGACTGAGGAGAGAAATCGCTTGAACCC	60		
DB	8122	TGGCAGCGCGCTGTAGTCCCGCTACTCAGGAGCTGAGGAGAGAAATCGCTTGAACCT	8063		
QY	61	GGGAGCAGCGAGGTTCAGTGAGCCCAAGATCGCGTCACTGCCAGCTCCGCGGACA---	117		
DB	8062	GGGAGCAGCGAGGTTCAGTGAGCTGAGATTCACCACTGCACTCCAGCTCCGCAACAAG	8003		
QY	118	-GACGTTCCGTTTCAAGAGAAAAAATAATATATAAAGAAATAAATATCGGCGCTGC	176		
DB	8002	CGAGACTCGCTCTCAAAAAAATAAATAATAATAATAATAATAATAATAATAATAATA	7943		
QY	177	CGCGT 181			
DB	7942	ATGGT 7938			
RESULT 2					
US-09-820-003A-28					

US-09-764-847-1738

Query Match 11.2% Score 112.4; DB 10; Length 2147;
Best Local Similarity 79.0%; Pred. No. 5.9e-21;
Matches 147; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 1 TGGCACGGCCCTGTAGTCCAGCTACTCAGGAGACTGAGGCAGGAGAAATCGTTGAACCC 60
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Db 99 TGGCACGGCCCTGTAAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATGCTTTGAACCC 158
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QY 61 GGGAGACGGAGGTTTCAGTGTAGCCAAAGATCGCGTCACTGCACCTCCAGCTGGCGACAG-- 118
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Db 159 AGGAGGCGGAGGTTGCATGAGCCAAAGATCAGCCCACTGCACCTCCAGCTGGTGACAGAG 218
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QY 119 -ACGTTCCGTTTCAAAGAAAAATAATATTAATAAAAAAGATAAAAAATCCGCGCTGGC 177
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Db 219 CAAGACTCTGCTCAAAAAAATAAAAAATCAGTAAAAATGTTAAACATTTGGGGAATCT 278
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QY 178 CGGTGA 183
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Db 279 GGTGA 284

RESULT 8
US-09-876-216-3
; Sequence 3, Application US/09876216
; Patent No. US2002081689A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN DEHYDROGENASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN DEHYDROGENASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000906
; CURRENT APPLICATION NUMBER: US/09/876,216
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

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; LENGTH: 14485
; TYPE: DNA
; ORGANISM: Human
US-09-876-216-3

Query Match      11.2%; Score 112.2; DB 10; Length 14485;
Best Local Similarity 82.2%; Pred. No. 1.9e-20;
Matches 129; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Db 2776 TGGCAGGTGCGCTGTAGTCCCACTACTCAGGAGGCTGAGCGAGGAGAATCACTTGAACCC 2835

QY 61 GGGAGACGGAGGTTGCATGTAGCCCAAGATCGCGTCTCACTGCATCCAGCCTGGCGCAGAC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2836 GGGAGCGGAGGTTGCATGTAGCCCAAGATTTGGCCCACTGCATCCAGCCTCGTGACAGAG 2895

QY 121 GTTCGTTTCAAAAGAAAAATAATATTATAAAAA 157
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2896 CAGAAATCCCTCTCAAAAAGAAAAAAGAAAAAAA 2932

RESULT 9
US-09-880-107-3428/c
; Sequence 3428, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2002, 21:54:28 ; Search time 32.3575 Seconds
(without alignments)
12277.043 Million cell updates/sec

Title: US-09-708-724A-3_COPY_10000_11000

Perfect score: 1001

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Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications_NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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c 2	76	7.6	302250	10	US-09-962-832-154
c 3	73.2	7.3	326014	10	US-09-731-231A-3
c 4	70.8	7.1	465237	10	US-09-933-267A-1
c 5	70.2	7.0	678	10	US-09-811-284-116
c 6	70	7.0	88191	10	US-09-799-799-3
c 7	69.4	6.9	560	10	US-09-822-246-3
c 8	66.6	6.7	197997	10	US-09-867-701-1522
c 9	65.8	6.6	32038	10	US-09-764-878-292
c 10	65	6.5	1400	10	US-09-263-959-299
c 11	65	6.5	684973	10	US-09-263-959-1
c 12	64.8	6.5	4409	10	US-09-764-869-2014
c 13	64.8	6.5	4494	10	US-09-764-869-2012
c 14	64.8	6.5	4495	10	US-09-764-869-2011
c 15	64.2	6.4	45845	10	US-09-927-091-6
c 16	63	6.3	465	10	US-09-864-761-5381
c 17	63	6.3	368004	10	US-09-949-654-3
c 18	62.6	6.3	503	10	US-09-783-590-7878
c 19	61.4	6.1	465237	10	US-09-933-267A-1

c 20	60.6	6.1	474	10	US-09-864-761-11163	Sequence 11163, A
c 21	60.6	6.1	80959	9	US-09-858-546-3	Sequence 3, Appli
c 22	60.4	6.0	29220	9	US-09-764-868-1312	Sequence 1312, Ap
c 23	60.4	6.0	29220	9	US-09-764-868-1313	Sequence 1313, Ap
c 24	59.6	6.0	88191	10	US-09-799-799-3	Sequence 3, Appli
c 25	59.4	5.9	26225	10	US-09-764-869-1276	Sequence 1276, Ap
c 26	59.4	5.9	99916	10	US-09-816-095-3	Sequence 3, Appli
c 27	59.2	5.9	66804	10	US-09-740-041-3	Sequence 3, Appli
c 28	59	5.9	13819	10	US-09-764-877-2596	Sequence 2596, Ap
c 29	59	5.9	13821	10	US-09-764-877-2595	Sequence 2595, Ap
c 30	58.6	5.9	2066	10	US-09-822-849A-78	Sequence 78, Appli
c 31	58.6	5.9	167343	10	US-09-962-436-281	Sequence 281, App
c 32	58.6	5.9	167343	10	US-09-964-824A-273	Sequence 273, App
c 33	58.4	5.8	208	10	US-09-867-701-8913	Sequence 8913, Ap
c 34	57.8	5.8	409	10	US-09-867-701-5909	Sequence 5909, Ap
c 35	56.8	5.7	381	10	US-09-867-701-2096	Sequence 2096, Ap
c 36	56.8	5.7	504	10	US-09-867-701-10604	Sequence 10604, A
c 37	56.8	5.7	6500	9	US-09-764-904-129	Sequence 129, App
c 38	56.8	5.7	6500	10	US-09-764-860-1190	Sequence 1190, Ap
c 39	56.2	5.6	56516	9	US-09-853-526-1	Sequence 1, Appli
c 40	56.2	5.6	56516	10	US-09-901-484A-1	Sequence 1, Appli
c 41	56.2	5.6	56520	9	US-09-853-526-179	Sequence 179, App
c 42	56.2	5.6	56520	10	US-09-901-484A-179	Sequence 179, App
c 43	56	5.6	26048	10	US-09-764-869-1556	Sequence 1556, Ap
c 44	56	5.6	397658	10	US-09-813-320-3	Sequence 3, Appli
c 45	55.8	5.6	2118	10	US-09-800-729-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1

US-09-949-654-3/c
; Sequence 3, Application US/09949654
; Patent No. US20020127644A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000817
; CURRENT APPLICATION NUMBER: US/09/949,654
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/231,572
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 368004
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(368004)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-654-3

Query Match	7.7%	Score 77.2;	DB 10;	Length 368004;
Best Local Similarity	68.5%;	Pred. No. 5e-09;		
Matches 137;	Conservative 0;	Mismatches 58;	Indels 5;	Gaps 2;
Qy 231	AAAAAGTTTAAATAGGACCTTAGGTGGTCTTAATCCAATCTAAGTGATCTGCC	290		
Db 33099	AGATCGAGTTAAATAGGTCATTAGGTGGGCTTATGCAATATGACTGGTGTCTC	33040		
Qy 291	ATGAAGAGGAATAAGGATACAAATGTGCACACAGAGAGAAATGGCCACATGAGGACAC	350		
Db 33039	ATAAAGAGGAGTAATTAGCACACAGA---CATGCGAGAGGGAAGACCATATTAAGACAC	32984		
Qy 351	AATGAGATGTGGCTACTTACAGCCTAGGAGAGAGGCTCGGAGAAAACACACCTTACC	410		
Db 32983	AGGGAGATAATGGC-ATCTACAAGCCAAAGGAAAGGCGCTCAGAGAAACACCTTTGCT	32925		


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RESULT 5
US-09-811-284-116/c
; Sequence 116, Application US/09811284
; Patent No. US20020058306A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US20020058306alel G Protein-Coupled Receptors
; FILE REFERENCE: 00167US1
; CURRENT APPLICATION NUMBER: US/09/811,284
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,783
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,907
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,918
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,960
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,917
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/192,945
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,916
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,923
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,933
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,830
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,234
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/192,155
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,935
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-284-116

Query Match      7.0%; Score 70.2; DB 10; Length 678;
Best Local Similarity 67.4%; Pred. No. 2e-08;
Matches 130; Conservative 0; Mismatches 58; Indels 5; Gaps 2;

Qy 240 TTAATAAGGAGCCTTAGGGTGGTCTTAATCCCAATCTAAGTGATGTCTCCATGA-AAGA 298
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 366 TTAATAAGGAGTCATTAAGATGGCCCTGATGGAGCATAACAGGTGCTCTTATAAGAAG 307

Qy 299 GGAATAAGGATACAAATGTCACACAGAGAGAAATGCCACATGAGGACACAATGAGAA 358
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 306 GGAGATTAGGACACAAA-----CACACACAGAGGGACGCCATGTGAAGACAGCAAGAA 251

Qy 359 TGTGGCTACTTACAGCCTAGGAGAGGCGCTCCGAGAAACACACACCTTACCCACACTT 418
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 250 GACGTCTCTGTGAGCCAGAGAGAGGCGCTCAGAGAAACCAAAACCTGCCGACACCTT 191

Qy 419 GATGTTGGACTTC 431
|||||  |||  |||  |||
Db 190 GATCATGAACATC 178

RESULT 6
US-09-799-799-3
; Sequence 3, Application US/09799799
; Patent No. US20020132291A1
; GENERAL INFORMATION:
; APPLICANT: Ye, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
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```
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001157
; CURRENT APPLICATION NUMBER: US/09/799,799
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 88191
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(88191)
; OTHER INFORMATION: n = A,T,C or G
US-09-799-799-3

Query Match      7.0%; Score 70; DB 10; Length 88191;
Best Local Similarity 62.6%; Pred. No. 1.8e-07;
Matches 134; Conservative 0; Mismatches 65; Indels 15; Gaps 1;

Qy 218 GTCAGTTACAATCAAAAAGTTTAAATAGAGACCTTAGGGTGGTCTTAATCCAAATCT 277
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 7364 GGCCTTTAAAGAGGTACAAAAGTTAAATAGAGTGGTCTCAGAGTGGTCTGTCTCAT 7423

Qy 278 AAGTGATGTCTCCATGAAGAGGAAATAAGGATACAAATGTCCACACAGAGAGAAATGCC 337
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 7424 GACTGGTGTCCAAAAGAGAG-----CTGAGGACTCACAGAGGGACAAC 7468

Qy 338 CACATGAGGACACAATGAGAATGTGGCTACTTACAAGCCTAGGAGAGAGCGCTCGAGAA 397
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 7469 CACGTGAGGACACAAGGATATGATGGTCTCTACAAGCAGGAGAGAGCGCTCAGGAGA 7528

Qy 398 AACACACCTTACCCACACCTTGATGTTGGACTTC 431
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 7529 AACCAACCTTCCCAACCTTGATCTCAGAGTTTC 7562

RESULT 7
US-09-867-701-1522/c
; Sequence 1522, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1522
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(560)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-1522

Query Match      6.9%; Score 69.4; DB 10; Length 560;
Best Local Similarity 67.5%; Pred. No. 2.9e-08;
Matches 129; Conservative 0; Mismatches 56; Indels 6; Gaps 2;

Qy 240 TTAATAAGGAGCCTTAGGGTGGTCTTAATCCCAATCTAAGTGATGTCTCCATGAAGAG 299
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 202 TTAATAAGGAGCCATTTGGTAGGTCTTAATCCAATATGACT--AGTATCCTTTATAAGAG 145

Qy 300 GAAATAAGGATACAAATGTGCACACAGAGAGAAATGCCACATGAGGACACAATGAGAA 359
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 144 GAGATTAGAACACACAGACTAG----TATAGGGGAAAGACCACTGTGAAGACACAGGGAGG 89
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Db 158 GTGTCCTTATC-----AGGAGGTAGGACACACAGCATGCAAGAGGGGAAGACCCAGAAAGAA 223
Qy 343 GAGGACACAATGAGAAATGGCTACTTACAAAGCCTAGGAGAGAGGCGCTCCGAGAAAAACAC 402
Db 224 GGTATAGAAAAAATAATTTGTTATCTACAAGCCCAAGGAGAGAGGCGCTCAGAGAAACCA 283
Qy 403 ACCCTAC 409
Db 284 ACTCAAC 290

RESULT 11
US-09-263-959-1
; Sequence 1, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-1
Query Match 6.5%; Score 65; DB 10; Length 684973;
Best Local Similarity 63.1%; Pred. No. 7.5e-06;
Matches 118; Conservative 0; Mismatches 65; Indels 4; Gaps 1;
Qy 223 TTCAATCAAAAAAGTTTAAATGAGGACCTTAGGGTGGCTCTTAATCCCAATCTAAGTG 282
Db 544708 TTACATCGATAATTAAGTTAAATTAAGTTCATTAGGTGGGCCCTAATTCATATGACTG 544767
Qy 283 ATGCTCCTCAATGAAGAGAAATAGGATACAAATGTGCACACAGAGAGAAATGGCCACAT 342
Db 544768 GTGTCCTTATC-----AGGAGGTAGGACACACAGCATGCAAGAGGGGAAGACCCAGAAAGAA 544823
Qy 343 GAGGACACAATGAGAAATGGCTACTTACAAAGCCTAGGAGAGAGGCGCTCCGAGAAAAACAC 402
Db 544824 GGTATAGAAAAAATAATTTGTTATCTACAAGCCCAAGGAGAGAGGCGCTCAGAGAAACCA 544883
Qy 403 ACCCTAC 409
Db 544884 ACTCAAC 544890

RESULT 12
US-09-764-869-2014/c
; Sequence 2014, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2014
; LENGTH: 4409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2014
Query Match 6.5%; Score 64.8; DB 10; Length 4409;
Best Local Similarity 63.0%; Pred. No. 1e-06;
Matches 121; Conservative 0; Mismatches 62; Indels 9; Gaps 1;
Qy 240 TTAATAAGGATACAAATGTGCACACAGAGAGAAATGGCCACATGAGGACACAATGAGAAT 299
Db 3801 TTAATAAGTTCATCTAGGTGGGCCCAATCCAAGATGACTGGTGTCTCTTTTG----- 3748
Qy 300 GAAATAAGGATACAAATGTGCACACAGAGAGAAATGGCCACATGAGGACACAATGAGAAT 359
Db 3747 ---GGAACAGGAGACTAGTGCACACAGAGAGAAAGGCGCTGAGGACACACTGGACAG 3691
Qy 360 GTGGCTACTTACAAAGCCTTAGGAGAGAGGCGCTCCGAGAAAAACACACCCCTACACACCTTG 419
Db 3690 ACGGCCACCTCGAAGCCAAAGGGAGGGCGCTCAGAAGACATCAAACTTAAGGATAACTTG 3631
Qy 420 ATGTTGGACTTC 431
Db 3630 ATCTTGCACTTC 3619
RESULT 13
US-09-764-869-2012/c
; Sequence 2012, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 2012
; LENGTH: 4494
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2012
Query Match 6.5%; Score 64.8; DB 10; Length 4494;
Best Local Similarity 63.0%; Pred. No. 1e-06;
Matches 121; Conservative 0; Mismatches 62; Indels 9; Gaps 1;
Qy 240 TTAATAAGGATACAAATGTGCACACAGAGAGAAATGGCCACATGAGGACACAATGAGAAT 299
Db 3801 TTAATAAGTTCATCTAGGTGGGCCCAATCCAAGATGACTGGTGTCTCTTTTG----- 3748
Qy 300 GAAATAAGGATACAAATGTGCACACAGAGAGAAATGGCCACATGAGGACACAATGAGAAT 359
Db 3747 ---GGAACAGGAGACTAGTGCACACAGAGAGAAAGGCGCTGAGGACACACTGGACAG 3691
Qy 360 GTGGCTACTTACAAAGCCTTAGGAGAGAGGCGCTCCGAGAAAAACACACCCCTACACACCTTG 419

GenCore version 5.1.3
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Listing first 45 summaries

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					40: em_htgo_mus:									
					41: em_htgo_other:									

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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No.		Score		Match		%					
1	229.4	18.4	151049	9	AC018558	Homo sapi				AC018558	Homo sapi
2	229.4	18.4	191768	9	AC092357	Homo sapi				AC092357	Homo sapi
3	203.4	16.3	191014	9	AC113268	Papio cyn				AC113268	Papio cyn
4	192	15.4	153629	9	AC092325	Homo sapi				AC092325	Homo sapi
5	183.2	14.7	125133	9	HSBG8211	Human DNA				AL109799	Human DNA
6	173.8	14.0	185664	2	AC093249	Homo sapi				AC093249	Homo sapi
7	173.8	14.0	207538	2	AC106886	Homo sapi				AC106886	Homo sapi
8	173	13.9	124047	9	AL713966	Human DNA				AL713966	Human DNA
9	173	13.9	131234	9	HS172K2	Human DNA				284814	Human DNA
10	173	13.9	160623	9	AL670296	Human DNA				AL670296	Human DNA
11	169	13.6	183165	9	AP000802	Homo sapi				AP000802	Homo sapi
12	169	13.6	184841	9	AC016902	Homo sapi				AC016902	Homo sapi
13	169	13.6	185569	2	AP003099	Homo sapi				AP003099	Homo sapi
14	168.8	13.6	7736	9	AF079797	Homo sapi				AF079797	Homo sapi
15	168.8	13.6	35715	9	AC020951	Homo sapi				AC020951	Homo sapi
16	168.8	13.6	178184	9	AC008770	Homo sapi				AC008770	Homo sapi
17	168.8	13.6	179272	2	AC069149	Homo sapi				AC069149	Homo sapi
18	168.8	13.6	179581	2	AC009397	Homo sapi				AC009397	Homo sapi
19	166.2	13.3	178053	2	AC021112	Homo sapi				AC021112	Homo sapi
20	165.6	13.3	184539	2	AC027192	Homo sapi				AC027192	Homo sapi
21	165.6	13.3	192087	2	AC079325	Homo sapi				AC079325	Homo sapi
22	165.6	13.3	201306	2	AC087390	Homo sapi				AC087390	Homo sapi
23	165.6	13.3	206143	2	AC069390	Homo sapi				AC069390	Homo sapi
24	164.6	13.2	36430	9	AC010506	Homo sapi				AC010506	Homo sapi
25	163.8	13.2	121287	9	AC010332	Homo sapi				AC010332	Homo sapi
26	163.8	13.2	184169	2	AC026349	Homo sapi				AC026349	Homo sapi
27	163.8	13.2	219553	2	HS312687	Homo sapi				AJ312687	Homo sapi
28	163.6	13.1	187280	2	AC092674	Homo sapi				AC092674	Homo sapi
29	163.6	13.1	207962	2	AC051664	Homo sapi				AC051664	Homo sapi
30	162.2	13.0	160169	2	AC051664	Homo sapi				AC051664	Homo sapi
31	160.8	12.9	24020	9	HS7269L11	Human DNA				AL049740	Human DNA
32	160.8	12.9	130819	9	AL662842	Human DNA				AL662842	Human DNA
33	160.6	12.9	48993	9	AC104527	Homo sapi				AC104527	Homo sapi
34	160.6	12.9	159849	2	AC021454	Homo sapi				AC021454	Homo sapi
35	160.6	12.9	163915	2	AC087451	Homo sapi				AC087451	Homo sapi
36	160.6	12.9	166867	9	AF003733	Homo sapi				AF003733	Homo sapi
37	160.6	12.9	174305	2	AC074126	Homo sapi				AC074126	Homo sapi
38	160.6	12.9	231247	9	AC008543	Homo sapi				AC008543	Homo sapi
39	160	12.9	143068	6	AX335952	Sequence				AX335952	Sequence
40	160	12.9	143068	9	HS095626	Homo sapien				U95626	Homo sapien
41	160	12.9	220965	2	HS312688	Homo sapi				AJ312688	Homo sapi
42	159	12.8	37392	9	AC005946	Homo sapi				AC005946	Homo sapi
43	159	12.8	143619	9	AC008812	Homo sapi				AC008812	Homo sapi
44	159	12.8	185437	9	AC098613	Homo sapi				AC098613	Homo sapi
45	159	12.8	190628	2	AC024700	Homo sapi				AC024700	Homo sapi

ALIGNMENTS

RESULT 1
AC018558
LOCUS AC018558 Homo sapiens chromosome 16 clone RP11-80F22, complete sequence.
DEFINITION AC018558 Homo sapiens chromosome 16 clone RP11-80F22, complete sequence.
ACCESSION AC018558
VERSION AC018558.5 GI:16596530
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 151049)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished

REFERENCE	2 (bases 1 to 151049)	DOE Joint Genome Institute.
AUTHORS	DOE Joint Genome Institute.	
TITLE	Sequencing of Human Chromosome 16	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 191768)	DOE Joint Genome Institute.
AUTHORS	DOE Joint Genome Institute.	
TITLE	Direct Submission	
JOURNAL	Submitted (03-JUL-2001)	Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE	3 (bases 1 to 151049)	DOE Joint Genome Institute.
AUTHORS	DOE Joint Genome Institute.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-NOV-2001)	Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT	On Nov 2, 2001 this sequence version replaced gi:9795566.	
	Sequence Quality Assessment:	
	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.	
	All manually edited bases have been reduced to quality zero.	
	Quality levels above 40 are expected to have less than 1 error in 10,000 bp.	
	Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.	

	Sequence Quality Assessment:	
	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.	
	All manually edited bases have been reduced to quality zero.	
	Quality levels above 40 are expected to have less than 1 error in 10,000 bp.	
	Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.	

FEATURES	Location/Qualifiers	
source	1..151049	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/chromosome="16"	
	/clone="RP11-80F22"	
BASE COUNT	46827 a 30783 c 30749 g 42690 t	
ORIGIN		
	Query Match 18.4%; Score 229.4; DB 9; Length 151049;	
	Best Local Similarity 97.5%; Pred. No. 2.8e-47;	
	Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
QY	692 CCAGGAGCCATGTTCTGAATCTCAAAATTTGAAGAATCTTTGTCCTCCACCCACACAC 751	
Db	133275 CGAGGAGCCATGTTCTGAATCTCAAAATTTGAAGAATCTTTGTCCTCCACCCACACAC 133334	
QY	752 CCAAGAAAATAATAACAGGAGGAGGAGGATGAAAATTTGGCGTCTACACCCCTCCAG 811	
Db	133335 CCAAGAAAATAATAACAGGAGGAGGAGGATGAAAATTTGGCGTCTACACCCCTCCAG 133394	
QY	812 TAGCAGAAACCTGTACCATCTCCTTCAGTAACAGAAATAGAGACCCCTGCAAGAA 871	
Db	133395 TAGCAGAAACCTGTACCATCTCCTTCAGTAACAGAAATAGAGACCCCTGCAAGAA 133454	
QY	872 TTCCGCGGACTGCTACCATAGCTGGAGAGCCCTTAGGACATGCACTTTTCT 930	
Db	133455 TTCTATGCTCTGCTACCATAGCTGGAGAGCCCTTAGGACATGCACTTTTCT 133513	
RESULT 2		
LOCUS	AC092357 191768 bp DNA linear PRI 15-AUG-2001	
DEFINITION	Homo sapiens chromosome 16 clone RP11-332P24, complete sequence.	
ACCESSION	AC092357 AC023764	
VERSION	AC092357.2 GI:15187270	
KEYWORDS	HTG.	
SOURCE	Homo sapiens.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE	1 (bases 1 to 191768)	
AUTHORS	DOE Joint Genome Institute.	
TITLE	Sequencing of Human Chromosome 16	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 191768)	DOE Joint Genome Institute.
AUTHORS	DOE Joint Genome Institute.	
TITLE	Direct Submission	
JOURNAL	Submitted (03-JUL-2001)	Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT	On or before Aug 15, 2001 this sequence version replaced gi:7596817, gi:14589546.	
	Sequence Quality Assessment:	
	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.	
	All manually edited bases have been reduced to quality zero.	
	Quality levels above 40 are expected to have less than 1 error in 10,000 bp.	
	Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.	

	Sequence Quality Assessment:	
	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.	
	All manually edited bases have been reduced to quality zero.	
	Quality levels above 40 are expected to have less than 1 error in 10,000 bp.	
	Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.	

FEATURES	Location/Qualifiers	
source	1..191768	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/chromosome="16"	
	/clone="RP11-332P24"	
BASE COUNT	57149 a 39592 c 40150 g 54877 t	
ORIGIN		
	Query Match 18.4%; Score 229.4; DB 9; Length 191768;	
	Best Local Similarity 97.5%; Pred. No. 2.8e-47;	
	Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
QY	692 CCAGGAGCCATGTTCTGAATCTCAAAATTTGAAGAATCTTTGTCCTCCACCCACACAC 751	
Db	83020 CGCAGGAGCCATGTTCTGAATCTCAAAATTTGAAGAATCTTTGTCCTCCACCCACACAC 83079	
QY	752 CCAAGAAAATAATAACAGGAGGAGGATGAAAATTTGGCGTCTACACCCCTCCAG 811	
Db	83080 CCAAGAAAATAATAACAGGAGGAGGATGAAAATTTGGCGTCTACACCCCTCCAG 83139	
QY	812 TAGCAGAAACCTGTACCATCTCCTTCAGTAACAGAAATAGAGACCCCTGCAAGAA 871	
Db	83140 TAGCAGAAACCTGTACCATCTCCTTCAGTAACAGAAATAGAGACCCCTGCAAGAA 83199	
QY	872 TTCCGCGGACTGCTACCATAGCTGGAGAGCCCTTAGGACATTTGCACTATTCT 930	
Db	83200 TTCTATGCTCTGCTACCATAGCTGGAGAGCCCTTAGGACATTTGCACTATTCT 83258	
RESULT 3		
LOCUS	AC113268/c 191014 bp DNA linear PRI 14-AUG-2002	
DEFINITION	Papio cynocephalus anubis clone rp41-22m16, complete sequence.	
ACCESSION	AC113268	
VERSION	AC113268.8 GI:22095124	
KEYWORDS	HTG.	
SOURCE	olive baboon.	

```

ORGANISM      Papio cynocephalus anubis
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
               Cercopithecinae; Papio.
REFERENCE     1 (bases 1 to 191014)
AUTHORS      Zhou,L., Fu,Y., Wu,J., Eichler,E. and Roe,B.A.
TITLE        Papio anubis BAC Clone rp41-22m16
JOURNAL      Unpublished
REFERENCE     2 (bases 1 to 191014)
AUTHORS      Zhou,L., Fu,Y., Wu,J., Eichler,E. and Roe,B.A.
TITLE        Direct Submission
JOURNAL      Submitted (06-AUG-2002) Department of Chemistry And Biochemistry,
               The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
               OK 73019, USA
REFERENCE     3 (bases 1 to 191014)
AUTHORS      Zhou,L., Fu,Y., Wu,J., Eichler,E. and Roe,B.A.
TITLE        Direct Submission
JOURNAL      Submitted (06-AUG-2002) Department of Chemistry And Biochemistry,
               The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
               OK 73019, USA
REFERENCE     4 (bases 1 to 191014)
AUTHORS      Zhou,L., Fu,Y., Wu,J., Eichler,E. and Roe,B.A.
TITLE        Direct Submission
JOURNAL      Submitted (14-AUG-2002) Department of Chemistry And Biochemistry,
               The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
               OK 73019, USA
COMMENT      On Aug 4, 2002 this sequence version replaced gi:21104942.
               ----- Genome Center
               Center: Department of Chemistry And Biochemistry
               The University Of Oklahoma
               Center code:UOKNOR
               -----

FEATURES             Location/Qualifiers
     source           1..191014
                     /organism="Papio cynocephalus anubis"
                     /sub_species="anubis"
                     /db_xref="taxon:9555"
                     /clone_lib="rp41-22m16"
                     /clone_lib="RP41 - 41 Male (Olive) Baboon BAC Library"
BASE COUNT      54882 a 40134 c 39560 g 56438 t
ORIGIN
Query Match      16.3%; Score 203.4; DB 9; Length 191014;
Best Local Similarity 91.1%; Pred. No. 1.2e-40;
Matches 216; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 694 CAGAGCCATGTTCTGAATCTCAAAATTTGAAAGAAATCTTTTGTCCACCCACACACCC 753
      |||||||
Db 122104 CAGGAGCCATGTTCTGAATCTCGAAATTTTGAAGAGTCTTTTGTCCACCCACACACCC 122045

QY 754 AAGAAAAATATAACAGGAGGAGGAGTGAATAATGGCGTCTACACACCCCTCCAGTA 813
      |||||||
Db 122044 GATGAATAATATAACAGGAGGAGGAGTGAATAATGGCGTCTGACACCCCTCCAGTA 121985

QY 814 GCAGAAACACCTGTACCATCTCTTCAGTAAACAGAAATAGAGACCCCTCCAGAAATTT 873
      |||||||
Db 121984 GCAGAAACACCTGTATCATCTCTTCAGTAAACAGAAATAGAGACCCCTCCAGAAATTT 121925

QY 874 CCGGGGACTGCTACCATAGCTGGAGAGCCCTTAGGACATTCACATTTCT 930
      |||||||
Db 121924 ATATGCTTTGCTGCCATAGCTGGAGAGCCCTTAGGACATTCACATTTCT 121868

RESULT 4
AC092325/c      153629 bp DNA linear PRI 02-NOV-2001
LOCUS           Homo sapiens chromosome 16 clone RP11-14K3, complete sequence.
DEFINITION      AC092325 AC011682
ACCESSION       AC092325.2 GI:16596537
VERSION         HTG.
KEYWORDS        Homo sapiens.
SOURCE          Homo sapiens
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 153629)
AUTHORS      DOE Joint Genome Institute.
TITLE        Sequencing of Human Chromosome 16
JOURNAL      Unpublished
REFERENCE     2 (bases 1 to 153629)
AUTHORS      DOE Joint Genome Institute.
TITLE        Direct Submission
JOURNAL      Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE     3 (bases 1 to 153629)
AUTHORS      DOE Joint Genome Institute.
TITLE        Direct Submission
JOURNAL      Submitted (02-NOV-2001) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT      On or before Nov 2, 2001 this sequence version replaced gi:7329393,
               gi:14589514.
               ----- Sequence Quality Assessment:
               This entry has been annotated with sequence quality
               estimates computed by the Phrap assembly program.
               All manually edited bases have been reduced to quality zero.
               Quality levels above 40 are expected to have less than
               1 error in 10,000 bp.
               Base-by-base quality values are not generally visible from the
               GenBank flat file format but are available as part
               of this entry's ASN.1 file.
               -----
               ----- Sequence Quality Assessment:
               This entry has been annotated with sequence quality
               estimates computed by the Phrap assembly program.
               All manually edited bases have been reduced to quality zero.
               Quality levels above 40 are expected to have less than
               1 error in 10,000 bp.
               Base-by-base quality values are not generally visible from the
               GenBank flat file format but are available as part
               of this entry's ASN.1 file.
               -----

FEATURES             Location/Qualifiers
     source           1..153629
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="16"
                     /clone="RP11-14K3"
BASE COUNT      45079 a 31598 c 31052 g 45900 t
ORIGIN
Query Match      15.4%; Score 192; DB 9; Length 153629;
Best Local Similarity 100.0%; Pred. No. 9.4e-38;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1054 CAGCAGAAACCATGAGCCTAGCGGACGCGGCTTCGGAAGCTCCCTCCGCAACG 1113
      |||||||
Db 129738 CAGCAGAAACCATGAGCCTAGCGGACGCGGCTTCGGAAGCTCCCTCCGCAACG 129679

QY 1114 GGCCTCTCTCAGACCGCTCGTGCCTCCGCTCCGCGGAGCTGACCGCAGCGAGTGA 1173
      |||||||
Db 129678 GGCCTCTCTCAGACCGCTCGTGCCTCCGCTCCGCGGAGCTGACCGCAGCGAGTGA 129619

QY 1174 GAGTTGCTCTCTGTTGGCGGTGACACGAGGAGGACTGGAGCGCGGATCATCTCCAGGA 1233
      |||||||
Db 129618 GAGTTGCTCTCTGTTGGCGGTGACACGAGGAGGACTGGAGCGCGGATCATCTCCAGGA 129559

QY 1234 CGGCTGAGTAG 1245
      |||||||
Db 129558 CGGCTGAGTAG 129547

RESULT 5
HSBG8211        125133 bp DNA linear PRI 16-DEC-2000
LOCUS           Human DNA sequence from clone GS1-8211 on chromosome Xq26.3-27.3
DEFINITION      Contains a pseudogene similar to Novel human gene mapping to
               chromosome X, gene for LDOC1 protein, ESTs, SsTs, GSSs and a CpG

```



```
consensus"
55571..55864
/note="ALUSg1 repeat: matches 1..294 of consensus"
55866..56210
/note="match: GSS: Em:AQ310669"
complement(join(56599..56669,57317..57592))
/note="match: STS: Em:AA412270"
56677..57126
/note="LTR46 repeat: matches 1..461 of consensus"
complement(57127..57499)
/note="match: GSS: Em:AQ390433"
59073..59927
/note="LIM1 repeat: matches -1389..-530 of consensus"
60584..60929
/note="LIM48 repeat: matches 5937..6289 of consensus"
63785..64322
/note="LTR25-internal repeat: matches 3797..4338 of
consensus"
64318..64584
/note="MER4-internal repeat: matches 2241..2494 of
consensus"
64589..64668
/note="LTR8 repeat: matches 157..253 of consensus"
64674..64966
/note="MERS1-internal repeat: matches 3973..4273 of
consensus"
64903..66811
/note="MER41-internal repeat: matches 1826..3447 of
consensus"
65578..67242
/note="HURS-P3b repeat: matches 5213..6885 of consensus"
67618..70203
/note="LIM1 repeat: matches 858..3409 of consensus"
76561..76610
/note="25 copies 2 mer tt 78% conserved"
complement(77362..77634)
/note="match: GSS: Em:AQ731675"
77643..78226
/note="match: GSS: Em:AQ489768"
77671..78133
/note="match: GSS: Em:AQ285114"
78300..78420
/note="LIP3 repeat: matches 6024..6144 of consensus"
79742..80106
/note="LIP7 repeat: matches 5777..6141 of consensus"
82916..83206
/note="LIP15 repeat: matches 5838..6149 of consensus"
85946..87158
/note="LIMB7 repeat: matches 4936..6168 of consensus"
87490..88402

Query Match      14.7%; Score 183.2; DB 9; Length 125133;
Best Local Similarity 86.0%; Pred. No. 1.6e-35;
Matches 203; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 694 CAGGAGCCATGTCGAATCTCAAAATTTGAAGAATCTTTGTCCCAACACACACC 753
DB 100433 CAGGAGTCATGCTCGAGCTAAATTTAAAGAATCTTTGTCCCAACACATCA 100492

QY 754 AAAGAAAATAAACAAGAGGAGGAGGATGAAATTTGGCGTCTACCCCTCCAGTA 813
DB 100493 ATTAATAATAAACAAGAGGAGGAGGATGAAATTTGGCGTCTACCCCTCCAGTA 100552

QY 814 GCAGAAACACCTGTACCATCTCTTCAGTAACAGAAATAGAGACCCCACTGCAAGAATT 873
DB 100553 GCAGAAACATCTGTACCACTCTTCAGTAACAGAAATAGAGACCCCACTGCAAGAATT 100612

QY 874 CGCGGACTGTACCATAGCTGGAGGCCCTTAGGACATTTGCATTTTCACTATTTTC 929
DB 100613 TTACGCTCTGCTATAGCTGGAGGCCCTTAGGACATTTGCATTTTCCCATTTTC 100668
```

RESULT 6

```
AC093249
LOCUS
DEFINITION
AC093249
ACCESSION
VERSION
AC093249.3 GI:18481999
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 185664)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
DOE Joint Genome Institute.
2 (bases 1 to 185664)
DOE Joint Genome Institute.
Direct Submission
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 185664)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 3, 2002 this sequence version replaced gi:15383791.
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
-----
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
-----
FEATURES
Location/Qualifiers
source
1..185664
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-146F11"
BASE COUNT 45014 a 47979 c 46282 g 46389 t
ORIGIN

Query Match      14.0%; Score 173.8; DB 9; Length 185664;
Best Local Similarity 86.1%; Pred. No. 4.1e-33;
Matches 204; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 694 CAGGAGCCATGTCGAATCTCAAAATTTGAAGAATCTTTGTCCCAACACACACC 753
DB 83718 CAGGAGCCATGTCGAATCTCAAAATTTCAAGAATCTTTGTCCCTCCACAGGCC 83777

QY 754 AAAGAAAATAAACAAGAGGAGGAGGATGAAATTTGGCGTCTACCCCTCCAGTA 813
DB 83778 ATTG-AAATATAACAAGAGGAGGAGGATGAAATTTGGCTGTACCCCTCCAGTA 83836

QY 814 GCAGAAACACCTGTACCATCTCTTCAGTAACAGAAATAGAGACCCCACTGCAAGAATT 873
DB 83837 GTGGACACACGTGTACTGCTCTCTTCAGTAACAGAAATAGAGACCCCAACAGAAAT 83896

QY 874 CGCGGACTGTACCATAGCTGGAGGCCCTTAGGACATTTGCATTTTCACTATTTCT 930
DB 83897 CTACGCTCTGCTGCCATAGCTGGAGGCCCTTCGAACCTTTGTGCTTTTCTATTCT 83953
```


ORIGIN

Query Match 13.9%; Score 173; DB 9; Length 124047;
Best Local Similarity 83.1%; Pred. No. 6.4e-33;
Matches 197; Conservative 0; Mismatches 40; Indels 0;

QY	594	CAGGAGCCATGTTCTGAATCTCAAAATTTTGAAGAAATCTTTTGTGCCACCACAAACACC	753
Db	12578	CAGGAGTGATGTTCTGTAGTCTAAAAATCTGAATAAATCTGTGTGCCACCACACAGCTCCA	12519
QY	754	AAAGAAAATAATAAACAGGAGAGAGGAGGATGAAAATTTGGCGTCTTACCACCCCTCCACGTA	813
Db	12518	ATTGAAAATAAAACACAGGAGAGGAGGATAAAATTTGGCCCTATACCACCTTCTTCCAATA	12459
QY	814	GCAGAAACACCTGTACCATTCTCTTCAGTACACAAAATAGAGACCCCACTGCCAAGAATT	873
Db	12458	GCAGAACATCTGTACTGCTCTCTCGTAGCAGCAATAGAGACCCCAATACAGAGAATT	12399
QY	874	CCGGGCACTGCTACCATAGCTAGCTGGAGAGCCCTTAGACATTCGCATTTCACTATTCT	930
Db	12398	TTACACCTTGCTGCATAGCTGGAGAGCCCTTAGAGACTTCGCATTTTCTCTATTCT	12342

RESULT 9

HS172K2	131234 bp	DNA	linear	PRI 18-SEP-2001
LOCUS	Human DNA sequence from clone RP1-172K2 on chromosome 6p21.1-21.3.			
DEFINITION	Contains the HLA-DRB3, HLA-DRB9 and HLA-DRA genes for major histocompatibility complex class II DR beta 3*01012, beta 9 (pseudogene) and alpha and the 5' end of the BTNL2 gene encoding MHC class II associated butyrophilin-like 2. Contains a CpG island, ESTs, STSS and GSSs, complete sequence.			

FEATURES	
source	Location/Qualifiers
	1. .131234
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="6"
	/map="p21.1-21.3"
	/clone="RP1-172K2"
	/clone_lib="RPC1-1"
misc_feature	complement(806..1381)
repeat_region	/note="match: GSS: Em:AQ590387"
	931..1061
misc_feature	/note="t1MA8 repeat: matches 6161..6287 of consensus"
	complement(1039..1380)
misc_feature	/note="match: GSS: Em:AQ129245"
	complement(1171..1669)
misc_feature	/note="match: GSS: Em:AQ482825"
	1702..2203
repeat_region	/note="match: GSS: Em:AQ175556"
	2815..3118
repeat_region	/note="AluSg repeat: matches 1..304 of consensus"
	3185..3483
repeat_region	/note="t1MB6 repeat: matches 5523..5826 of consensus"
	3489..3565
repeat_region	/note="U1 repeat: matches 3..79 of consensus"
	3566..3697
repeat_region	/note="t1PB3 repeat: matches 6019..6150 of consensus"
	3722..4075
repeat_region	/note="t1MB8 repeat: matches 5812..6173 of consensus"
	4112..4418
repeat_region	/note="AluSg1 repeat: matches 2..306 of consensus"
	4422..4734
repeat_region	/note="AluSg repeat: matches 1..309 of consensus"
	4802..5215
misc_feature	/note="XSTB repeat: matches 1..426 of consensus"
	complement(5283..5736)
misc_feature	/note="match: GSS: Em:AQ720841"
	complement(5344..5741)
repeat_region	/note="match: GSS: Em:AQ518823"
	5422..6132
misc_feature	/note="t1M4 repeat: matches 3339..4077 of consensus"
	5998..6383
misc_feature	/note="match: GSS: Em:B89913"
	6031..6383
misc_feature	/note="match: GSS: Em:AQ808102"
	join(6037..6327,21346..21450)
repeat_region	/note="match: GSS: Em:AQ226840"
	6187..6536
misc_feature	/note="t1M4 repeat: matches 1515..1911 of consensus"
	6390..6579
misc_feature	/note="match: GSS: Em:B89913"
	6390..6484
repeat_region	/note="match: GSS: Em:AQ808102"
	6537..6849
repeat_region	/note="AluJb repeat: matches 1..312 of consensus"
	6850..6928
repeat_region	/note="t1M4 repeat: matches 1911..1989 of consensus"
	7367..8132
repeat_region	/note="t1M4 repeat: matches 2110..2873 of consensus"
	8133..8427
repeat_region	/note="AluSg repeat: matches 1..290 of consensus"
	8429..8682
repeat_region	/note="AluY repeat: matches 1..254 of consensus"
	8693..8871
repeat_region	/note="AluY repeat: matches 7..185 of consensus"
	8872..8967
repeat_region	/note="AluY repeat: matches 216..307 of consensus"
	8968..9186
repeat_region	/note="t1M4 repeat: matches 2873..3090 of consensus"
	9187..9481
repeat_region	/note="AluSp repeat: matches 1..301 of consensus"

repeat_region 9482..10338
/note="L1M4 repeat: matches 3090. .4067 of consensus"
repeat_region 10347..11410
/note="L1M2 repeat: matches 4268. .5120 of consensus"
repeat_region 11411..11709
/note="AluY repeat: matches 1. .295 of consensus"
repeat_region 11710..11974
/note="L1M2 repeat: matches 5120. .5387 of consensus"
repeat_region 11975..12715
/note="L1R12 repeat: matches 40. .1523 of consensus"
repeat_region 12724..13852
/note="HERV9 repeat: matches 7281. .8399 of consensus"
repeat_region 13842..15313
/note="HERV9 repeat: matches 1730. .3199 of consensus"
repeat_region 15316..16837
/note="HERV9 repeat: matches 1. .1522 of consensus"
repeat_region 16838..17404
/note="L1R12 repeat: matches 1. .560 of consensus"
repeat_region 17407..17957
/note="L1M2 repeat: matches 5567. .6122 of consensus"
repeat_region 18022..18115
/note="L1M4 repeat: matches 7885. .7977 of consensus"
repeat_region 18139..18317
/note="L1M2/D repeat: matches 5465. .5657 of consensus"
repeat_region 18346..18601
/note="L1M2 repeat: matches 6057. .6313 of consensus"
misc_feature 18406..18673
/note="match: GSS: Em:AQ388150"
repeat_region 18673..19646
/note="L1R5 repeat: matches 1. .969 of consensus"
repeat_region 19879..20143
/note="MER51B repeat: matches 3. .266 of consensus"
repeat_region 20146..20627
/note="L1M2 repeat: matches 5567. .6057 of consensus"
repeat_region 20632..21122
/note="LOR1b repeat: matches 1. .497 of consensus"
repeat_region 21126..21331
/note="L1M2 repeat: matches 6062. .6260 of consensus"
repeat_region 21332..21639
/note="AluYa5 repeat: matches 1. .308 of consensus"
misc_feature 21640..21934
/note="match: GSS: Em:AQ231450"
repeat_region 21640..21694
/note="L1M2 repeat: matches 6260. .6315 of consensus"
repeat_region 21787..22733
/note="MER52A repeat: matches 270. .1239 of consensus"
repeat_region 23452..23523
/note="36 copies 2 mer tt 75% conserved"
repeat_region 23525..23667
/note="AluDb repeat: matches 161. .311 of consensus"
repeat_region 24292..24481
/note="MIR repeat: matches 51. .243 of consensus"
repeat_region 24918..25221
/note="AluY repeat: matches 1. .302 of consensus"
gene 26169..39233
/gene="HLA-DRB3"
mRNA join(26169..26304,33986..34255,36530..36811,37496..37606,
38080..38103,38903..39233)
/gene="HLA-DRB3"
/product="DJ172K2.6 (major histocompatibility complex,
class II, DR beta 3*01012)"
/note="match: CDNAS: Em:X03069 Em:E00199 Em:V00522
Em:A06800 Em:M7155 Em:M27635
match: ESTs: Em:AI750149 Em:AA443496 Em:W52776 Em:AA411478
Em:AA292976 Em:AA319703 Em:AA573731 Em:AA715935
Em:AI701955 Em:AI440139 Em:AA858441 Em:AI567982
Em:AI660611 Em:AI635249
/evidence="not_experimental"
misc_feature join(26205..26304,33986..34255,36530..36811,37496..37606,
38080..38103,38903..38926)
/gene="HLA-DRB3"
/note="match: STS: Em:G28562"
CDS join(26205..26304,33986..34255,36530..36811,37496..37606,

38080..38103,38903..38916)
/gene="HLA-DRB3"
/note="match: proteins: Tr:P79483"
/codon_start=1
/evidence="not_experimental"
/product="DJ172K2.6 (major histocompatibility complex,
class II, DR beta 3*01012)"
Query Match 13.9%; Score 173; DB 9; Length 131234;
Best Local Similarity 83.1%; Pred. No. 6.4e-33;
Matches 197; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 694 CAGGAGCCATGTTCTGAATCTCAAAATTTTGAAGAATCTTTTGTCCACCCACACACCC 753
||||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56534 CAGGAGTGTATGTTCTGAGTCTAAAAATCTGAAAAAATCTGTTGTCCACCCACAGCTCCA 56593
QY 754 AAAGAAAAATAAACAAGAGAGGAGGATGAAATTTGGCGTCTACCAACCCCTCCAGTA 813
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 56594 ATTGAAATATAAACAAGAGAGGAGGATGAAATTTGGCGTCTATACCACTCTCCAATA 56653
QY 814 GCAGAAACACCTGTACCATCTCTTTCAGTAACAGAAATAGAGACCCCACTGCAAGAAAT 873
||||| ||||||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56654 GCAGAAACATCTGTACTGCTCTCTTCGGTAGCAGAAATAGAGACCCCACTGAGAAAT 56713
QY 874 CGCGGACTGCTACCATAGCTGGAGAGCCCTTAGGACATTTGACATTTTCACTATTTCT 930
Db 56714 TTACACTCTGCTGCCATAGCTGGAGAGCCCTTGAGACCTTTTCCCTATTTCT 56770
RESULT 10
AL670296/c
LOCUS AL670296 160623 bp DNA linear PRI 24-APR-2002
DEFINITION Human DNA sequence from clone XxBac-213L12 on chromosome 6,
complete sequence.
ACCESSION AL670296
VERSION AL670296.7 GI:20135767
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
Tracey, A.
Direct Submission
Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 10, 2002 this sequence version replaced gi:19848110.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Swi:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep XxBac-213L12 is
from a CHORI-502 human bac - Cox cell line library VECTOR:
PTARBAC2.1
This sequence was generated from part of bacterial clone contigs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6/MHC.
LOCATION/Qualifiers
1. .160623

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="XXbac-213L12"
 /clone_lib="CHORI-502"
 BASE COUNT 47478 a 31913 c 32862 g 48370 t
 ORIGIN

Query Match 13.9%; Score 173; DB 9; Length 160623;
 Best Local Similarity 83.1%; Pred. No. 6.5e-33;
 Matches 197; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 694 CAGGAGCATGCTTCTGAATCTCAAATTTTGAAGAATCTTTGTGCCACCCACACACCC 753

Db 153404 CAGGAGTGATGCTTCTGAGTCTAAAAATCTGAAAAATCTGTGTGCCACCCACAGCTCCA 153345

QY 754 AAGAAATATAACAGGAGGAGGAGATGAAAAATTTGGGCTTACACCCCTCCAGTA 813

Db 153344 ATTGAAATATAAACAGGAGGAGGATGAAAAATTTGGGCTATACCACTCTCCCAATA 153285

QY 814 GCAGAACACCTGTACCATCTCCTTCAGTACAGAAATAGAGACCCCTGCAAGAAAT 873

Db 153284 GCAGAACATCTGTACTGCTCTCTCGTAGCAGAAATAGAGACCCCAATACAGAAAT 153225

QY 874 CCGGGAGCTGTACATAGCTGGAGACCCCTTAGGACATTTGCACCTTTCATTTCT 930

Db 153224 TTACACTCTGCTGCATAGCTGGAGACCCCTGAGGACCTTGCACTTTTCTATTCT 153168

RESULT 11
 AP000802/c

LOCUS 183165 bp DNA linear PRI 30-MAR-2001
 DEFINITION Homo sapiens genomic DNA, chromosome 11q, clone:RP11-629G13,
 complete sequences.

ACCESSION AP000802

VERSION AP000802.4 GI:13488765

KEYWORDS HTG.

SOURCE Homo sapiens DNA, clone:RP11-629G13.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (sites)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Homo sapiens genomic DNA

Published Only in DataBase (1999)

REFERENCE 2 (bases 1 to 183165)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (30-NOV-1999) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

[E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170]

On Mar 29, 2001 this sequence version replaced gi:10130031.

COMMENT

FEATURES

1..183165

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="11"

/map="11q"

/clone="RP11-629G13"

BASE COUNT 52120 a 36917 c 37962 g 56166 t

ORIGIN

Query Match 13.6%; Score 169; DB 9; Length 183165;

Best Local Similarity 84.4%; Pred. No. 6.8e-32;

Matches 190; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 707 CTGAATCTCAAAATTTTGAAGAATCTTTTGTGCCACCCACACACCAAGAAATAATA 766

Db 63869 CTGAATCTCAAAATTTTGAAGAATCTTTTGTGCCACCCACACAGCTCCCACTGAAAAATAAA 63810

QY 767 AACAGGAGGAGGAGTGAATAATTTGGGCTCTACCAACCCCTCCAGTAGCAGAAACACCTG 826
 Db 63809 AACAGGAGGAGGAGTGAATAATTTGGTCTATACGCCCTCCCTCCAGTTGCAGAAACATCTG 63750
 QY 827 TACCATCTCCTTCAGTAAACAGAAATAGAGACCCCACTGCAAGAAATTCGCGGACTGCTA 886
 Db 63749 TACCACCTCCTTCAGTAGCAGAAATAGAGACCCCACTGCAAGAAATTTTATACCTCTGCTG 63690
 QY 887 CCATAGCTGGAGAGCCCTTAGGACATTTGCACCTTTTCATATTTC 931
 Db 63689 CCATAGCTGGAGAGCCCTTAGGACCTTTGCACCTTTTCTATTTC 63645

RESULT 12
 AC016902/c

LOCUS 184841 bp DNA linear PRI 09-MAY-2001

DEFINITION Homo sapiens BAC clone RP11-217B19 from 11, complete sequence.

ACCESSION AC016902

VERSION AC016902.4 GI:11038566

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 184841)

Sulston,J.E. and Waterston,R.

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)

PUBMED 9847074

REFERENCE 2 (bases 1 to 184841)

Grewal,N., Maupin,R., Gregory,S. and O'Rourke,K.

The sequence of Homo sapiens BAC clone RP11-217B19

Unpublished

REFERENCE 3 (bases 1 to 184841)

Waterston,R.H.

Direct Submission

Submitted (08-DEC-1999) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

REFERENCE 4 (bases 1 to 184841)

Waterston,R.H.

Direct Submission

Submitted (30-OCT-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

REFERENCE 5 (bases 1 to 184841)

Waterston,R.

Direct Submission

Submitted (09-MAY-2001) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Oct 30, 2000 this sequence version replaced gi:7630895.

COMMENT

Center: Washington University Genome Sequencing Center

Web site: http://genome.wustl.edu/gsc

Contact: sapiens@wustl.wustl.edu

Summary Statistics

Center project name: H_NH0217B19

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is AC021387; the clone sequenced to the right is AP000802. Actual start of this clone is at base position 1 of RP11-217B19; actual end is at base position 184841 of RP11-217B19.

FEATURES

source

Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
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/clone="RP11-217B19"
/clone_lib="RPCI-11"
64..614
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681..999
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repeat_region

repeat_region

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repeat_region 15490..15603
/rpt_family="MIR"
repeat_region 16638..16850
/rpt_family="MaLR"
repeat_region 16968..17324
/rpt_family="MaLR"
repeat_region 18519..19702
/rpt_family="MER2_type"
19725..19797
/rpt_family="MIR"
repeat_region 20026..20314
/rpt_family="Alu"
repeat_region 20346..20442
/rpt_family="L1"
repeat_region 20561..20913
/rpt_family="L1"
repeat_region 22080..22390
/rpt_family="Alu"
repeat_region 22639..22772
/rpt_family="L2"
repeat_region 24130..24426
/rpt_family="Alu"
repeat_region 24508..24651
/rpt_family="MIR"
repeat_region 24980..25041
/rpt_family="MIR"
repeat_region 25831..25990
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25995..26163
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/note="similar to EST AI792363 (NID:g5340079) ov20b10.y5"
31216..31762
/note="similar to EST AI733639 (NID:g5054752) ov20b10.x5"
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repeat_region 32884..33138
/rpt_family="Alu"
repeat_region 33139..34100
/rpt_family="L1"
repeat_region 34147..34387
/rpt_family="CR1"
repeat_region 34494..34662
/rpt_family="MIR"
repeat_region 39266..39528
/rpt_family="Alu"
misc_feature 39913..40304
/note="similar to EST AI039230 (NID:g3278424) ox32e01.s1"
repeat_region 40122..40307
/rpt_family="MaLR"
repeat_region 40341..40478
/rpt_family="MaLR"
repeat_region 41462..41520
/rpt_family="MaLR"
repeat_region 41814..41941
/rpt_family="Alu"
repeat_region 44017..44122
/rpt_family="L2"
repeat_region 44198..44487
/rpt_family="MaLR"
repeat_region 44542..44912
/rpt_family="MaLR"
repeat_region 48201..48786
/rpt_family="ERV1"
repeat_region 49647..49817
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repeat_region 49818..50446
/rpt_family="ERV1"

Query Match 13.6%; Score 169; DB 9; Length 184841;
Best Local Similarity 84.4%; Pred. No. 6.8e-32;

Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.1.
SHGC-37302 G30664
Bases 17171 to 18499 excised as IS:Tn10.

FEATURES

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1. .35715
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="L1NLR-247E3"

BASE COUNT 9675 a 7687 c 8078 g 10275 t
ORIGIN

Query Match 13.6%; Score 168.8; DB 9; Length 35715;
Best Local Similarity 82.2%; Pred. No. 6.9e-32;
Matches 194; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 694 CAGGAGCCATGTTCTGAATCTCAAATTTGAAGAATCTTTGTCCACCCACACACCCC 753
Db 25727 CTGGAATCATATTTCTGAGTCTAAAAATCTGAAAGAATCTTTGTCCACCCACAGTACCA 25668
QY 754 AAAGAAAAATAATAACAGGAGGAGGAGATGAAAAATTTGGCGTCTTACCACCCCTCCAGTA 813
Db 25667 ACTGAAAAATAATAACAGGAGGAGGAGATGAAAAATTTGGCGTCTTACCACCCCTCCAGTA 25608
QY 814 GCAGAAACACCTGTACCATCTCCTTACGTACAGAAATAGAGACCCCACTGCAAAAGAAAT 873
Db 25607 GCAGAAACATCTGTACTGCTCCTTCGCTAGCAGAAATAGAGACCCCACTGCAAAAGAAAT 25548
QY 874 CCGGGAGTCTACCATAGCTGGAGAGCCCTTAGGACATTTGCACTTTTCACTATTTTC 929
Db 25547 TTATGCTCTGCTGCCATAGCTGGAGAGCCCTTAGGACCTTTGCGTTTTTTCCTATTTTC 25492

Search completed: December 24, 2002, 20:25:29
Job time : 3918.88 secs

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